# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 19:07:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525127.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10525127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525127.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 19:07:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525127.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 877,726 |
| Mapped reads | 772,652 / 88.03% |
| Unmapped reads | 105,074 / 11.97% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,260 / 2.42% |
| Read min/max/mean length | 30 / 101 / 101.89 |
| Duplicated reads (estimated) | 17,505 / 1.99% |
| Duplication rate | 1.35% |
| Clipped reads | 792,423 / 90.28% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,776,939 / 25.07% |
| Number/percentage of C's | 11,802,703 / 20.02% |
| Number/percentage of T's | 18,389,274 / 31.2% |
| Number/percentage of G's | 13,974,133 / 23.71% |
| Number/percentage of N's | 2,154 / 0% |
| GC Percentage | 43.73% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.019 |
| | |

| | |
|---|---|
| Standard Deviation | 0.214 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.43 |

## 2.5. Mismatches and indels

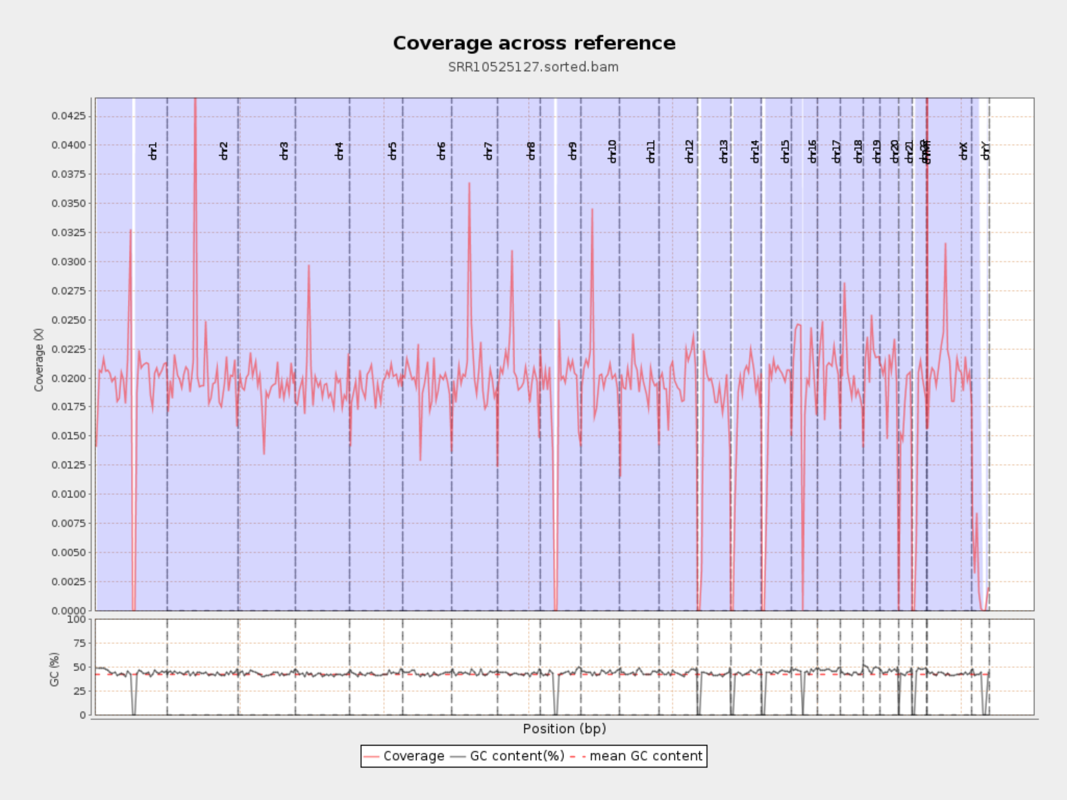
| | |
|---|---|
| General error rate | 0.79% |
| Mismatches | 452,670 |
| Insertions | 5,443 |
| Mapped reads with at least one insertion | 0.69% |
| Deletions | 13,776 |
| Mapped reads with at least one deletion | 1.76% |
| Homopolymer indels | 43.29% |

## 2.6. Chromosome stats

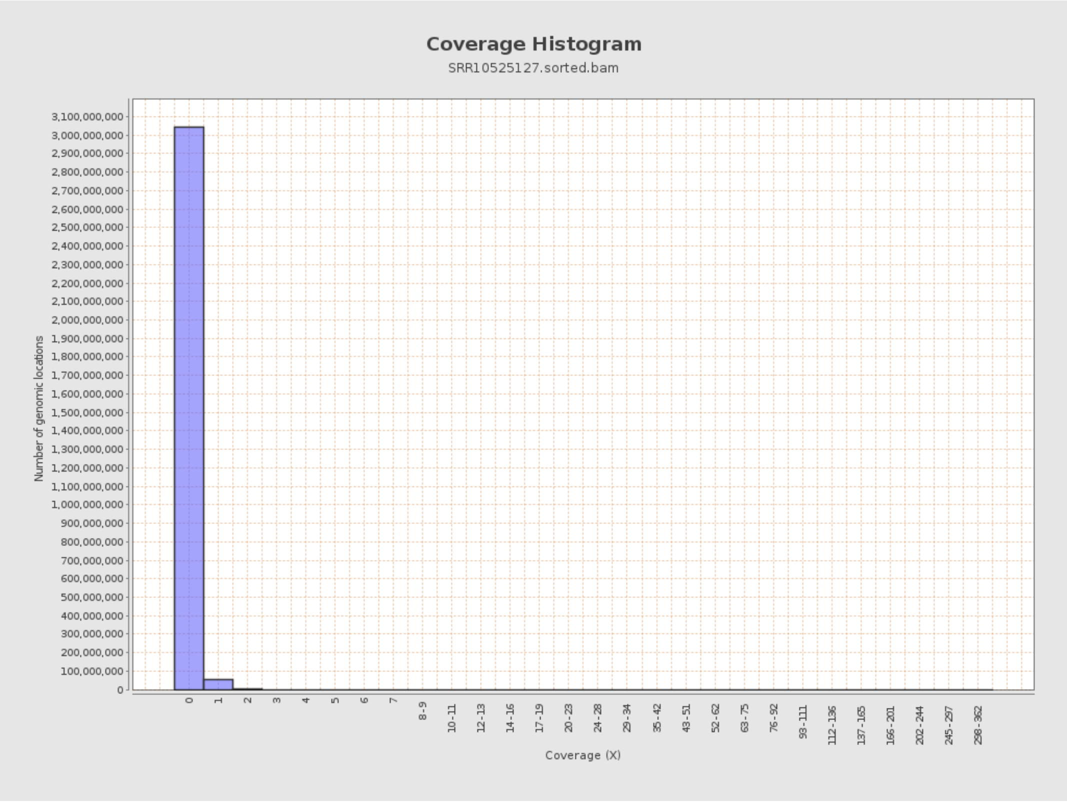
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4779833 | 0.0192 | 0.295 |
| chr2 | 243199373 | 5033903 | 0.0207 | 0.3208 |
| chr3 | 198022430 | 3839639 | 0.0194 | 0.1461 |
| chr4 | 191154276 | 3731872 | 0.0195 | 0.1565 |
| chr5 | 180915260 | 3532286 | 0.0195 | 0.1475 |
| chr6 | 171115067 | 3326365 | 0.0194 | 0.1596 |
| chr7 | 159138663 | 3287878 | 0.0207 | 0.2967 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3015402 | 0.0206 | 0.2749 |
| chr9 | 141213431 | 2502545 | 0.0177 | 0.2049 |
| chr10 | 135534747 | 2801386 | 0.0207 | 0.2124 |
| chr11 | 135006516 | 2664655 | 0.0197 | 0.2041 |
| chr12 | 133851895 | 2674590 | 0.02 | 0.149 |
| chr13 | 115169878 | 1823265 | 0.0158 | 0.1317 |
| chr14 | 107349540 | 1790661 | 0.0167 | 0.1508 |
| chr15 | 102531392 | 1718519 | 0.0168 | 0.1362 |
| chr16 | 90354753 | 1733513 | 0.0192 | 0.1538 |
| chr17 | 81195210 | 1704240 | 0.021 | 0.1728 |
| chr18 | 78077248 | 1575772 | 0.0202 | 0.3348 |
| chr19 | 59128983 | 1293616 | 0.0219 | 0.25 |
| chr20 | 63025520 | 1256626 | 0.0199 | 0.1505 |
| chr21 | 48129895 | 765905 | 0.0159 | 0.1398 |
| chr22 | 51304566 | 700485 | 0.0137 | 0.1226 |
| chrMT | 16571 | 1760 | 0.1062 | 0.3358 |
| chrX | 155270560 | 3256386 | 0.021 | 0.1846 |
| chrY | 59373566 | 158141 | 0.0027 | 0.0774 |

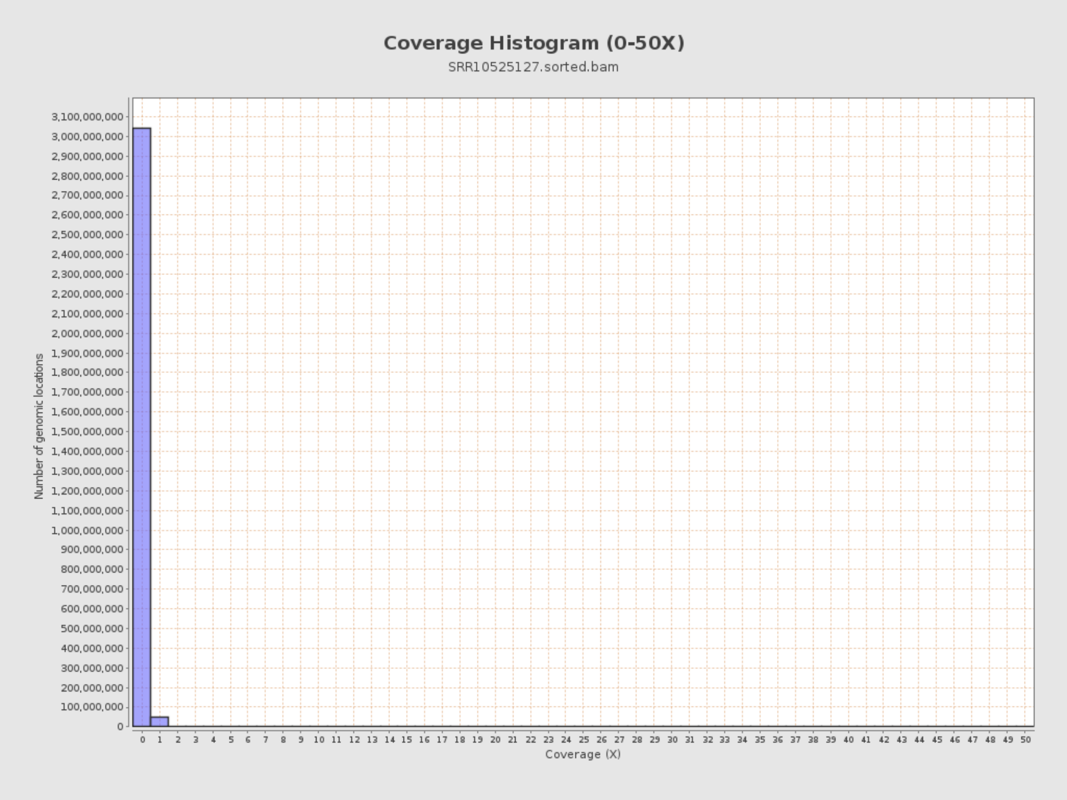
# 3. Results : Coverage across reference



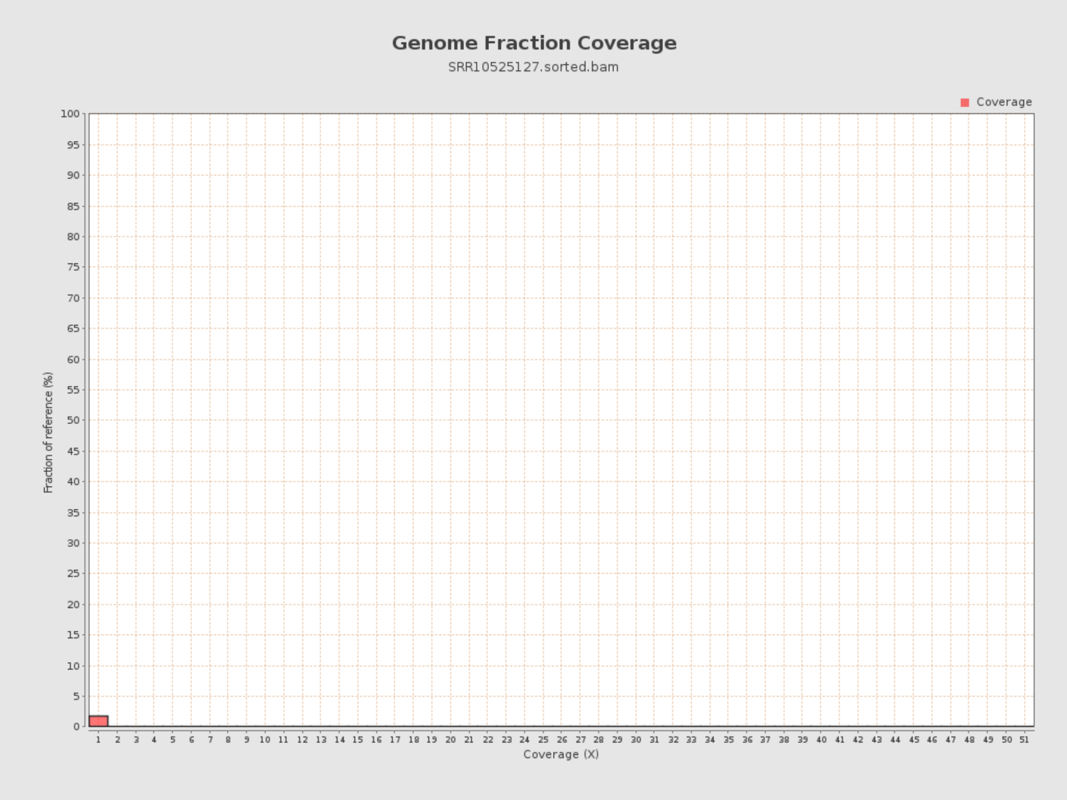
# 4. Results : Coverage Histogram



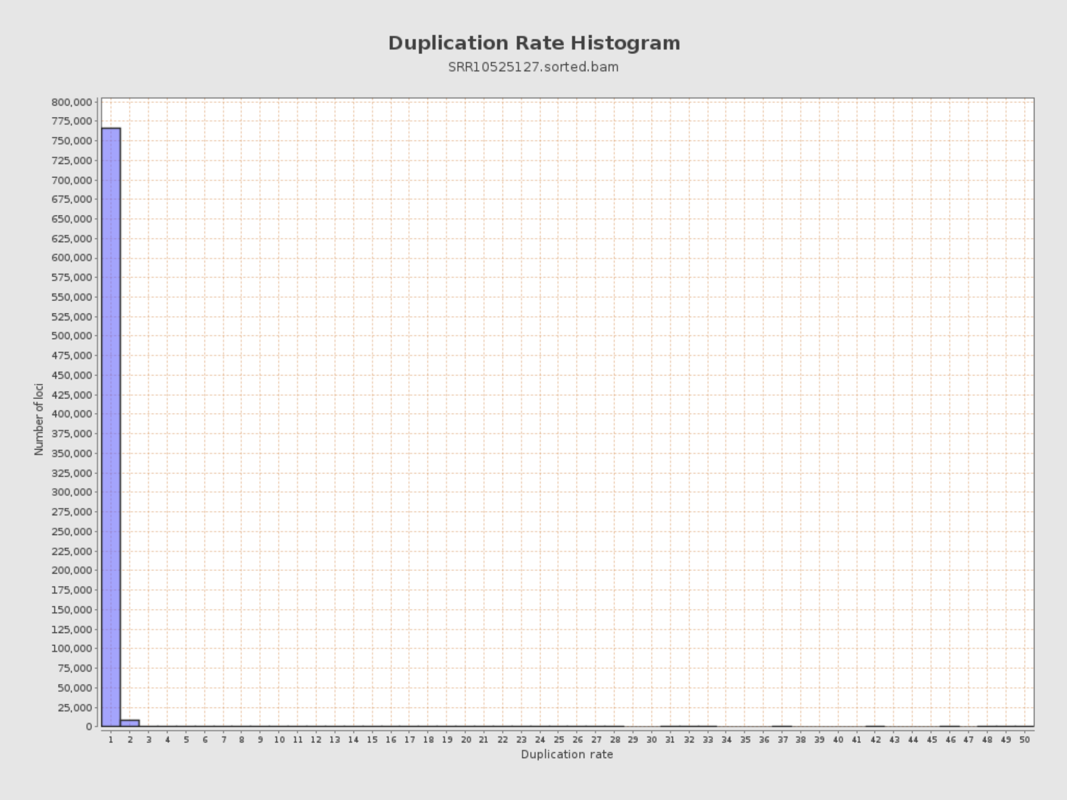
# 5. Results : Coverage Histogram (0-50X)



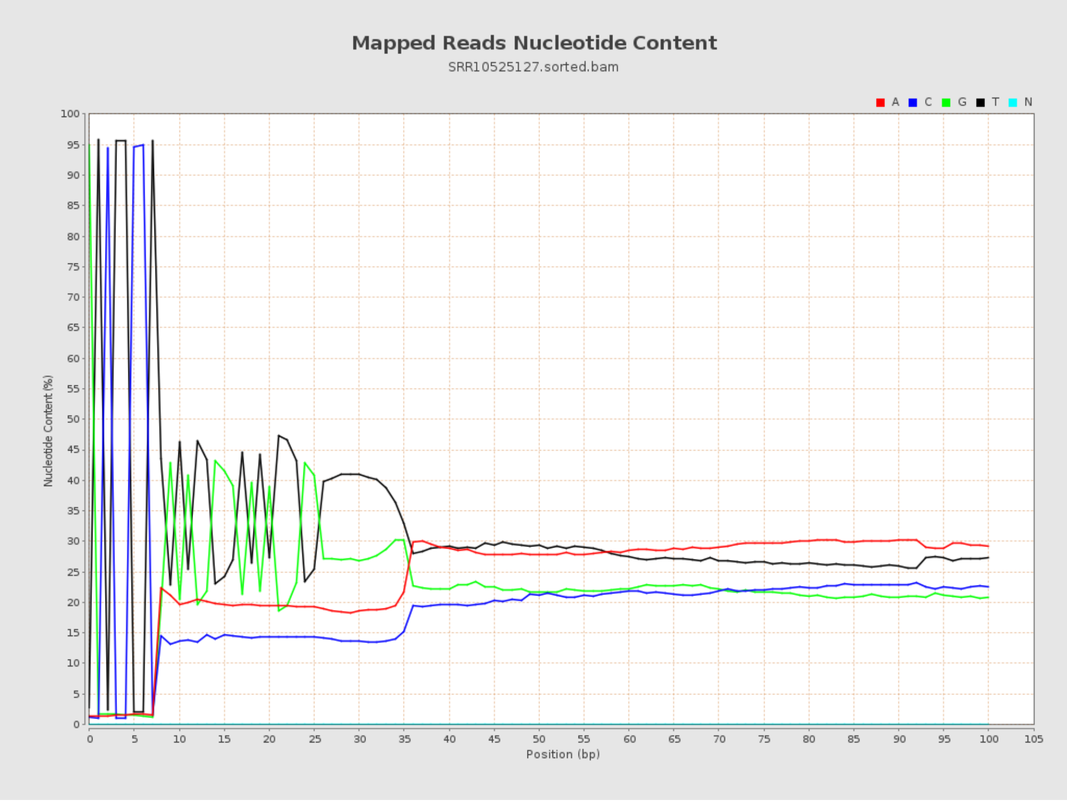
# 6. Results : Genome Fraction Coverage



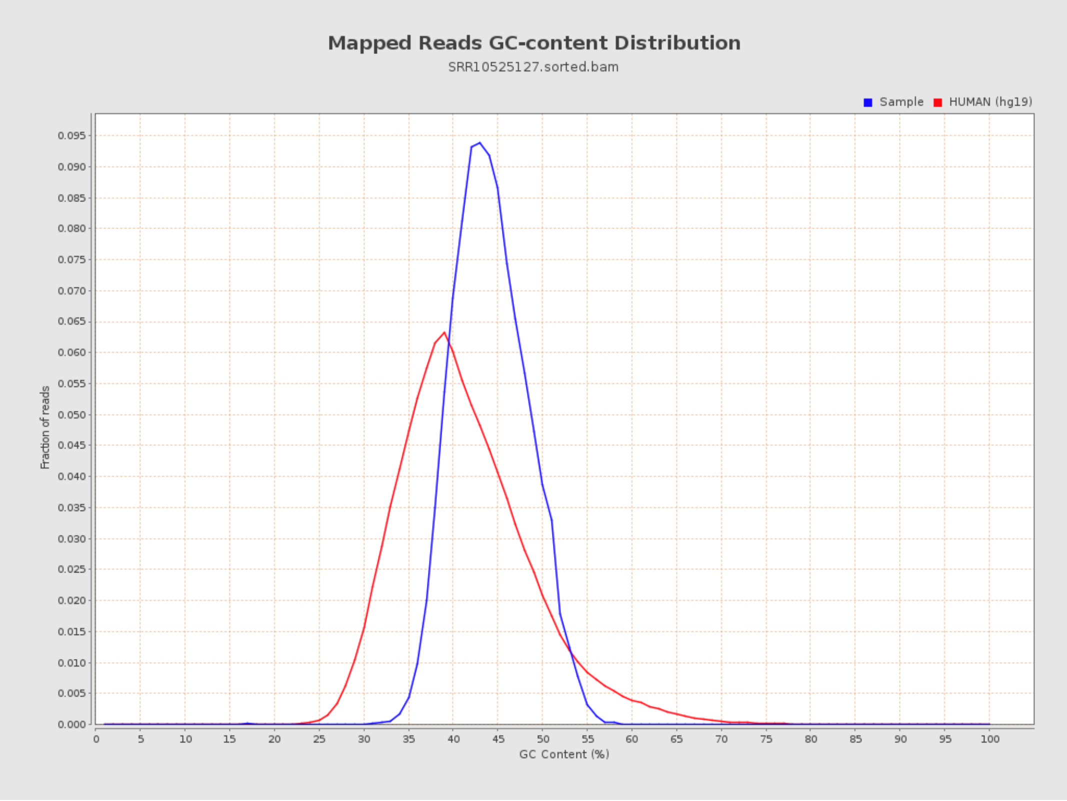
# 7. Results : Duplication Rate Histogram



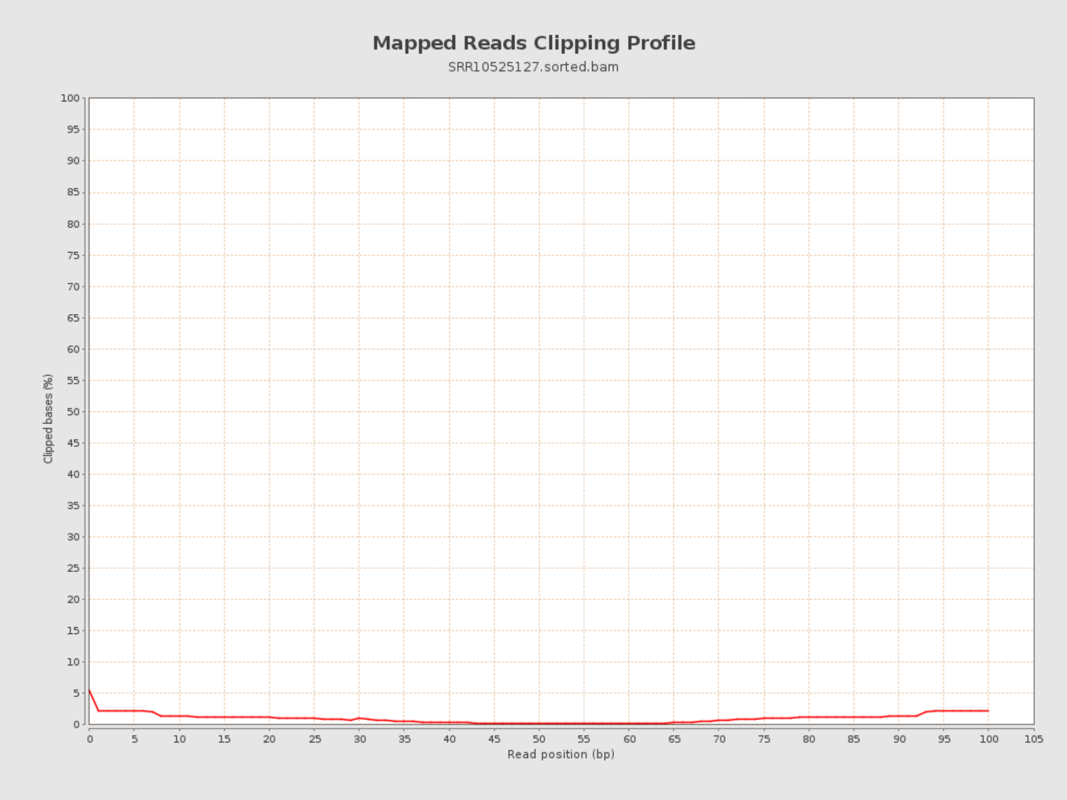
# 8. Results : Mapped Reads Nucleotide Content



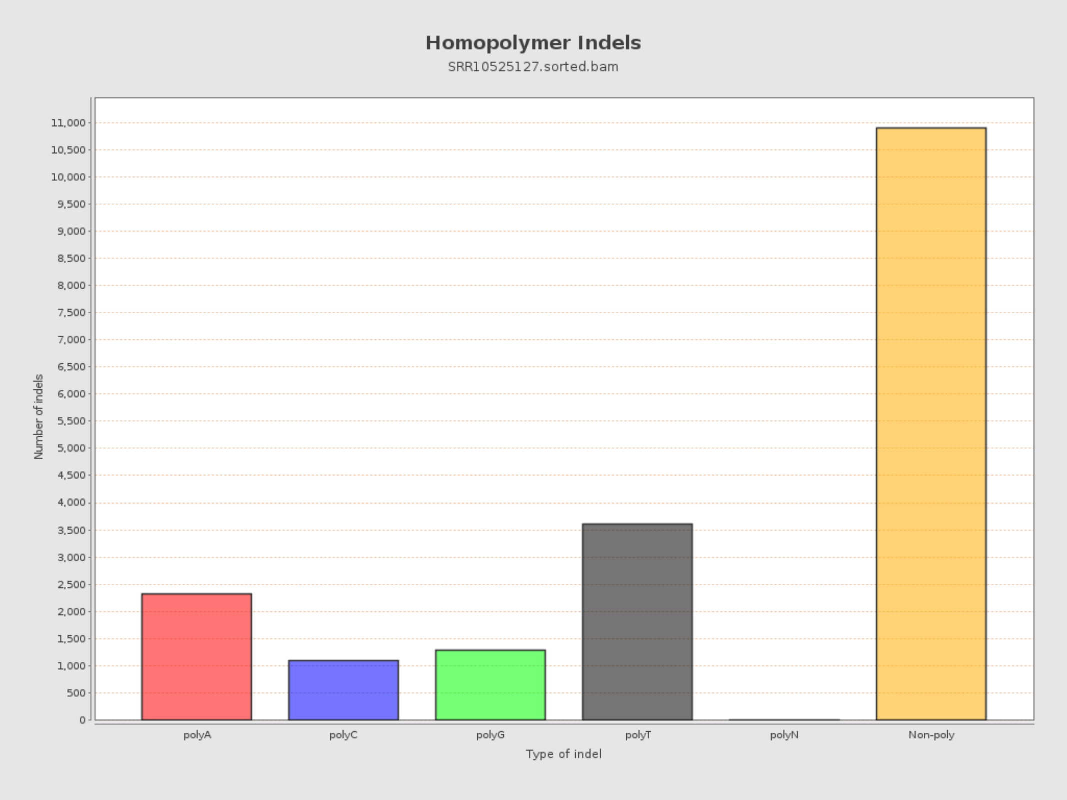
# 9. Results : Mapped Reads GC-content Distribution



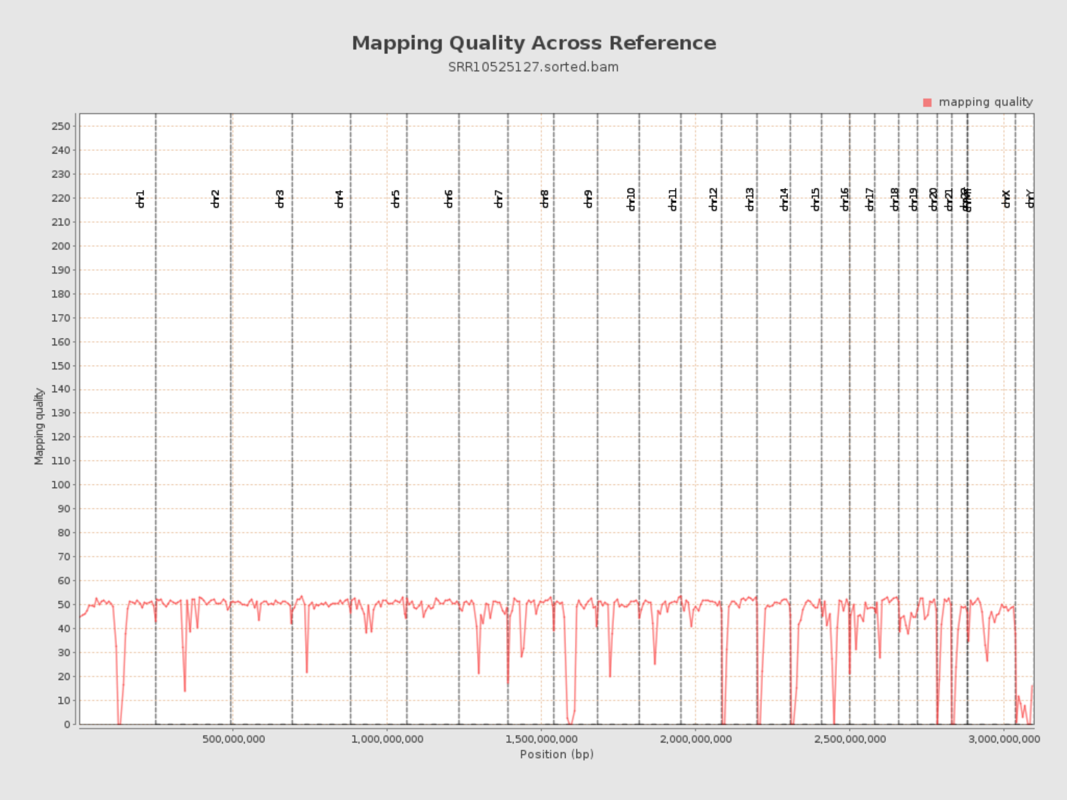
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram